


Form PTO 1449 US Department of Commerce Patent and Trademark Office 	ATTY CLIENT- MATTER NO: 66692-043 (P-TB 5072)	SERIAL NO. 10/040,895
	APPLICANT: Sem et al.	
INFORMATION DISCLOSURE STATEMENT BY APPLICANT	FILING DATE: 12/28/2001	GROUP: 1631 CONFIRMATION NO.: 1917

### U.S. PATENT DOCUMENTS

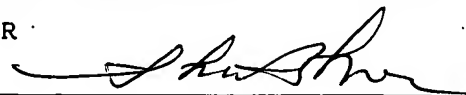
EXAM. INITIALS		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB- CLASS	FILING DATE

### FOREIGN PATENT DOCUMENTS

EXAM. INITIALS		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB- CLASS	TRANSLATION (YES/NO)
<i>JS</i>		WO 00/36096	6/22/00	PCT			
<i>JS</i>		WO 01/83717	11/8/01	PCT			

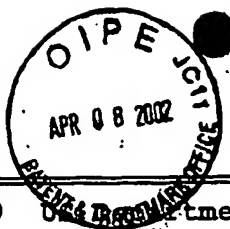
### OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages)

<i>JS</i>		Grundy and Bailey, "Family pairwise search with embedded motif models," Bioinformatics, 15:463-470 (1999)
<i>JS</i>		Jez et al., "Comparative anatomy of the aldo-keto reductase superfamily," Biochem. J 326:625-636 (1997)

EXAMINER 	DATE CONSIDERED 4/26/05
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EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.





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#### U.S. PATENT DOCUMENTS

EXAM. INITIALS	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB- CLASS	FILING DATE
<i>✓</i>	5,579,250	11/26/96	Balaji et al.			
<i>✓</i>	5,705,335	01/06/98	Hendry			
<i>✓</i>	5,888,738	03/30/99	Hendry			

#### FOREIGN PATENT DOCUMENTS

EXAM. INITIALS	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB- CLASS	TRANSLATION (YES/NO)
<i>✓</i>	WO 96/30849	1996				

#### OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages)

<i>✓</i>	Baldi and Brunak, <u>Bioinformatics: The Machine Learning Approach</u> , MIT Press, Cambridge MA, Chapters 4-9, pp. 73-215 (1998).
<i>✓</i>	Bladon, "A Rapid Method for Comparing and Matching the Spherical Parameter Surfaces of Molecules and Other Irregular Objects," <u>J. Mol. Graphics</u> , 7:130-137 (1989).
<i>✓</i>	Böhm, "Towards the Automatic Design of Synthetically Accessible Protein Ligands: Peptides, Amides and Peptidomimetics," <u>J. Comput.-Aided Mol. Des.</u> , 10:265-272 (1996).

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<i>A</i>	Brenner et al., "Understanding Protein Structure: Using <del>deep</del> for Fold Interpretation," <u>Meth. Enzymol.</u> , 266:635-643 (1996).
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<input checked="" type="checkbox"/>	Eddy, "Profile Hidden Markov Models," <u>Bioinformatics</u> , 14(9):755-763 (1998).
<input type="checkbox"/>	Everse et al., <u>The Pyridene Nucleotide Coenzymes</u> , Academic Press, Chapters 3-5, pp. 51-180 (1982).
<input type="checkbox"/>	Gribskov et al., "Profile Analysis: Detection of Distantly Related Proteins," <u>Proc. Natl. Acad. Sci. USA</u> , 84:4355-4358 (1987).
<input type="checkbox"/>	Hadley and Jones, "A Systematic Comparison of Protein Structure Classifications: SCOP, CATH and FSSP," <u>Structure</u> , 7:1099-1112 (1999).
<input type="checkbox"/>	Hubbard et al., "SCOP, Structural Classification of Proteins Database: Applications to Evaluation of the Effectiveness of Sequence Alignment Methods and Statistics of Protein Structural Data," <u>Acta. Cryst.</u> , D54:1147-1154 (1998).
<input type="checkbox"/>	Jaakkola et al., "A Discriminative Framework for Detecting Remote Protein Homologies," <u>J. Comput. Biol.</u> , 7:(1/2)95-114 (2000).
<input type="checkbox"/>	Kaufman and Rousseeuw, <u>Finding Groups in Data: An Introduction to Cluster Analysis</u> , Wiley-Interscience, 37-51 (1990).
<input type="checkbox"/>	Koradi et al., "MOLMOL: A Program for Display and Analysis of Macromolecular Structures," <u>J. Mol. Graphics.</u> , 14:51-55 (1996).
<input type="checkbox"/>	Kuntz et al., "A Geometric Approach to Macromolecule-Ligand Interactions," <u>J. Mol. Biol.</u> , 161:269-288 (1982).
<input type="checkbox"/>	Kutzenko et al., "Conserved Supersecondary Structural Motif in NAD-Dependent Dehydrogenases," <u>FEBS Lett.</u> , 423:105-109 (1998).
<input checked="" type="checkbox"/>	Marino et al., "J-Coupling Restraints in RNA Structure Determination," <u>Acc. Chem. Res.</u> , 32:614-623 (1999).

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<i>A</i>	Martin, "3D Database Searching in Drug Design," <u>J. Med. Chem.</u> , 35(12):2145-2154 (1992).
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<i>A</i>	Yang and Honig, "An Integrated Approach to the Analysis and Modeling of Protein Sequences and Structures. III. A Comparative Study of Sequence Conservation in Protein Structural Families Using Multiple Structural Alignments," <u>J. Mol. Biol.</u> , 301:691-711 (2000).

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